

XSB-001

APPENDIX B

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1 Scope

1.1 Identification

This manual is intended for the Restricted Rights release of the XSB, Inc. Generic Matcher software to **(insert client name here)**. This release is comprised of the following XSB Software elements:

<i>TITLE</i>	<i>VERSION</i>
Generic Matcher	1α

1.2 System Overview

The XSB, Inc. Generic Matcher software was developed to simplify the process of comparing two sets of objects based on their common attributes. The User supplies the Matcher with two sets of objects contained in a single ontology and then utilize the Matcher to create and edit match criteria to power the matching process.

The Generic Matcher has been under development at XSB, Inc. since July, 2002. XSB, Inc. maintains this software at its headquarters located at 25 East Loop Road, Stony Brook NY.

1.3 Document Overview

The purpose of this manual is to assist the user in the installation and responsible operation of the Generic Matcher software. This manual is protected by US copyright law and shall not be reproduced, duplicated, or distributed beyond **(insert client name here)** without the express written authorization and consent of XSB, Inc.

2 Referenced Documents

2.1 Documents Referenced by XSB

The XSB System is open-source in nature and can be freely down-loaded from the website:
<http://xsb.sourceforge.net/>.

The XSB system is a conservative extension of Prolog and includes powerful mechanisms for tabling, indexing and non-monotonic reasoning. The XSB system, along with Java are used as the major implementation platforms for the Generic Matcher.

3 Software Summary

3.1 Software Application

XSB's **Generic Matcher** is a JAVA and XSB based desktop tool that simplifies the process of comparing two sets of objects based on their common attributes. Matcher allows the user to create, edit match criteria and assign weights to different object attributes to configure the matching process.

Once the attribute matching is complete, Matcher allows users to either store results in the OMS format for additional processing or export the results to an MS Access table or a flat delimited file.

3.2 Software Inventory

REQUIRED SOFTWARE	
1. JRE version 1.4.1	
2. OS: Windows NT/2000/XP	

3.3 Software Environment

System Memory:	Recommended - 256 MB	Minimum - 128 MB
Free Disk Space:	Required – Approximately 100MB	
Processor Speed:	Recommended – PIII 500 Mhz	Minimum – PIII 300 Mhz

In addition, if you do not have Java Runtime Environment (JRE) V 1.4.0 or higher installed on your computer, you will need run the installer located in the "JRE" directory, which will be located on the software CD. Follow the instructions and prompts provided by the installation software.

Be sure to restart your computer after the installation has completed (the installer should prompt you to restart when finished).

3.4 Software Organization and Overview of Operation

The ODE Constructor Software provides:

- A graphical user interface to edit, create match criteria and invoke the matching process on two sets of objects.
- A color coded scheme to show in detail the results of the matching process.
- Pre-Defined matching functions that provide specialized comparison facilities for different data types.
- An import objects feature allowing users to import objects from a flat delimited file or MS Access table into the ontology.

Performance Characteristics:

- The Generic Matcher application currently accepts the following types of input:
Manual text inputs, Text files, MS Access files.
- Currently, Matcher writes output results to OMS files by default; however, the user has the ability to save match results in a flat delimited file or MS Access table.
- Typical program response time varies and is determined by a number of factors including the number of objects being compared, the size of the ontology being used, the efficiency of the matching functions and the limitations of the processor and ram of the user's computer.

3.5 Security and Privacy Protection

The XSB Generic Matcher software application and the related software documentation are distributed as Restricted Rights Software to **(insert client name here)**. Both the software code and the related software documentation are protected by US copyright law and may not be reproduced or distributed, in whole or in part, without the express written permission and authorization of XSB, Inc.

3.6 Assistance and Problem Reporting

Technical support is available through:

XSB, Inc.,
25 East Loop Road
Stony Brook, NY 11790
Voice: (631) 444-6800
Fax: (631) 444-6775
Email: support@xsb.com

4 Access to the Software

4.1 First Time Use of the Software

There is a batch file called "generic_matcher.bat" requiring 128MB of memory that runs the Generic Matcher application; to start and run the application, double-click the file referenced above.

Generic Matcher does offer users the ability to modify application settings and preferences but none of them have to be configured by the User at the start of the application.

4.2 Stopping or Suspending work – How to Interrupt Use of the Software and How to Determine Whether Normal Termination has Occurred.

A Generic Matcher session and its state can be saved to disk using the Save OMS item from the File menu pull down list; it can also be resumed at a later time by loading it back into the system using the Load OMS File menu item and providing the name of the directory where the OMS was previously saved.

It is recommended that, while working with the Generic Matcher, you periodically save the current OMS (which contains the state of the Matcher), in order to preserve your work. Since the software is still in alpha form, software bugs may cause the system to crash. If you have saved your work, after a crash you can restart from that point by re-executing the Generic Matcher and opening up the most recently saved version of the OMS.

It is also recommended that you periodically use "Save OMS As ..." to save a copy of the OMS in a new directory. Again this will allow you to restore your work to the point of saving. This is important to guard against software bugs that might corrupt the OMS, and against user errors that are not reversible or are not discovered until after an OMS has been saved.

***Note:** The Generic Matcher will prompt you with an exit warning screen each time you attempt to close the program to remind you to Save the OMS.

5 Processing Reference Guide

5.1 Processing Procedures –

Loading an existing Ontology –

To load an existing ontology select the Load OMS option from the File menu. You will then be prompted to select the directory where OMS is located; once you have selected the OMS, click the OK button to load the file into the Generic Matcher application.

This command removes any previously loaded OMS and loads in the new OMS. If you do not want to unload the previous OMS you can use the Merge OMS command. Other options available in this menu allow you to save the OMS. By saving the OMS you are also saving any match criteria you may have added or modified. The Save OMS Schema command lets you save the only the schema part of the OMS, this includes concepts, relationships and match criteria objects.

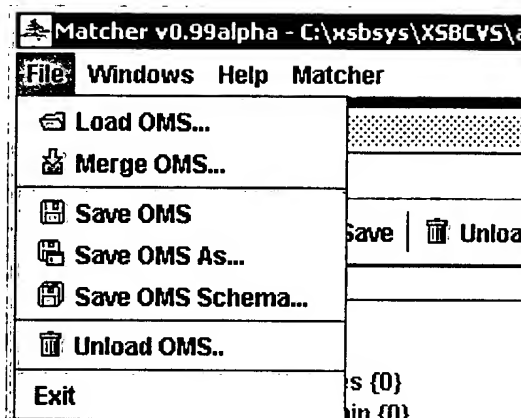


Fig. 1

Working with the Display Windows –

The main Generic Matcher display window is divided on two parts – the left panel, and the right panel. The left panel displays the currently loaded ontology; the right panel is used to create and edit match criteria.

Figure 2 below illustrates both the left and right panels. The right panel contains information about the attributes of the source and target classes while the left panel indicates what the source and target classes are and where they lie in the ontology.

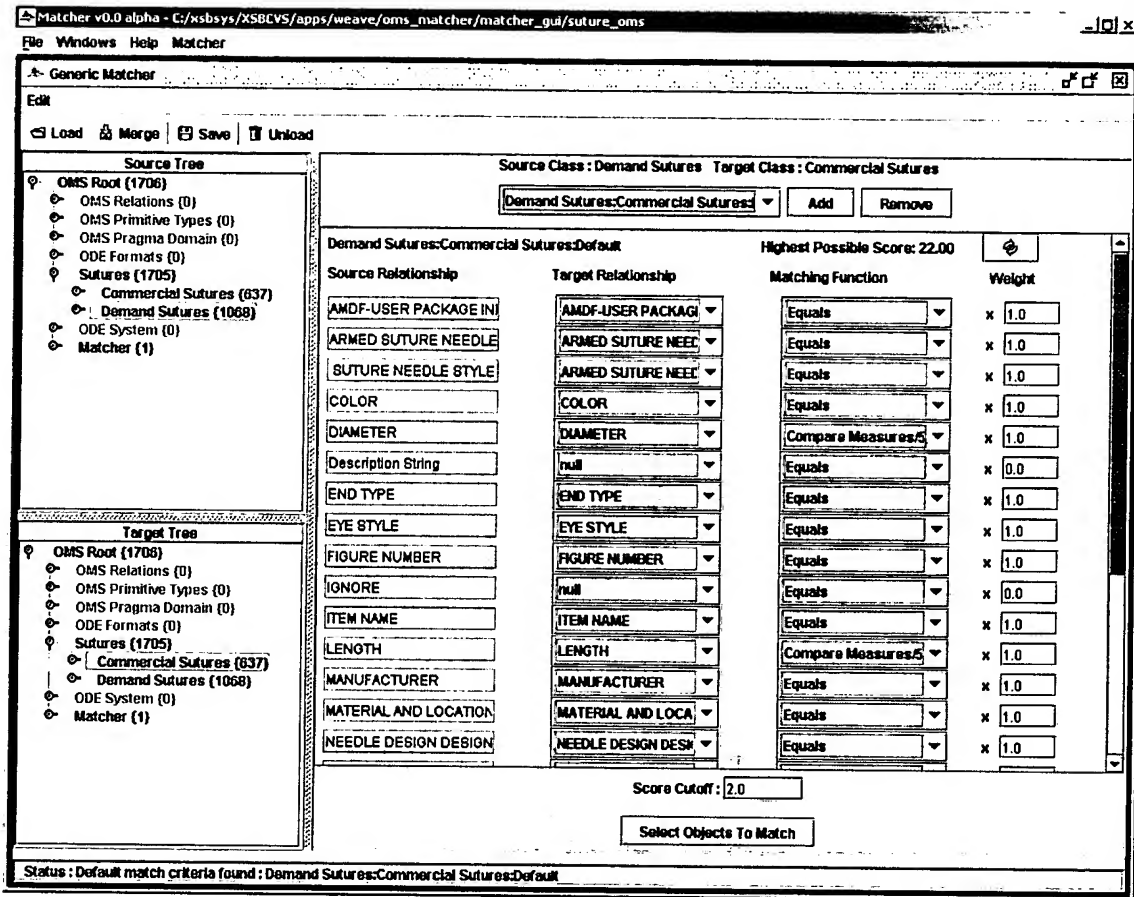


Fig 2

The left panel is split horizontally into two separate components each displaying the currently loaded ontology. The user begins the matching process by first selecting the source and target classes. The source class is chosen from the top tree and the target class is in the bottom tree (see Figure 3). The number next to the name of the class is the number of objects that are members of this class. The User can also view the relationships associated with this class by right clicking on the node and choosing the View Relationships option. Another option that is available when you right click on a node is the ability to import objects from a delimited flat file or database table. The User also has the ability to add new classes and relationship under this node. Once you have chosen both the target and source attribute the right panel of the main window will be rendered. At this point the matcher will try to find a stored default match criteria for these two classes. If it is found its settings will be displayed, otherwise the matcher will create a new default match criteria. This process can take some considerable time depending on the number of attributes under the source and target class and the limitations of the processor and ram.

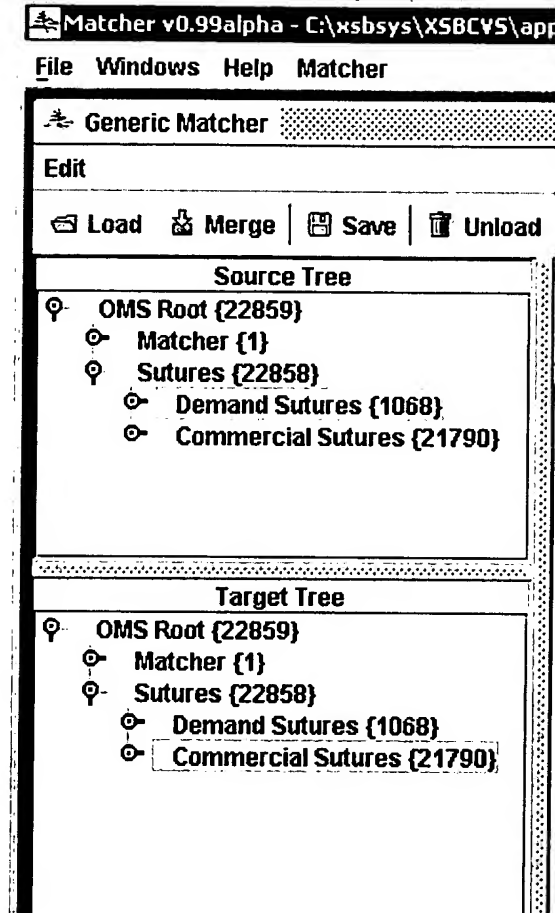


Fig 3

Managing match criterion –

The right panel is composed of three different components allowing the user to create, delete, and modify match criteria.

1. The top component allows the User to choose from the different match criteria associated with this pair of source and target classes. All pairs of source and target classes have a default match criteria associated with them. The default criteria can be modified but cannot be deleted.
 - a. Add Button: Creates a copy of the current match criterion and adds it to the drop down box. Once the button is clicked the matcher will prompt the User to name the new criteria. Once the match criterion has been named it will be set as the selected criteria in the drop down box. When a new match criterion is created the settings of the previous criterion are copied into the new one.
 - b. Remove Button: Deletes the currently selected match criterion in the drop down box.

Note: The User does not have the ability to delete the default match criterion.

- c. Drop down Box: Displays the currently selected match criteria. The settings associated with this match criteria are displayed in the middle component of the right panel. To change the match criteria just select it from the drop down box.
2. The middle component of the right panel contains the settings associated with the currently selected match criterion are displayed. There are four columns: Source relationship, Target Relationship, Matching Function and Weight.
 - a. Source Relationship: Relationship associated with the source class
 - b. Target Relationship: Relationships from the target class are of the same type as the source relationship. The User can choose from any one of the different choices available in the drop down box. To prevent the Matcher from comparing values of this attribute choose the null value in the drop down box.
 - c. Matching Function: Matching functions are specialized prolog predicates used by the matcher to compare values of a specific data type. The Generic Matcher has various built-in matching functions. The User can select from the different matching function available depending on the data type of the values being compared. The default matching function is the Equals matching function; it applies to all data types. It is the User's responsibility to choose the best and most efficient matching function for each attribute being compared. All matching functions return a score between the values of [-1.0, + 1.0].
 - d. Weight: Weights provide a way to give precedence to a particular attribute over others in the matching process. There is no set limit to what the User can set the weight to. An attribute with a weight of 0.0 is not compared.
 - e. Highest Possible Score: This is an aggregate of all the weights of all attributes being compared. To update this value the User must click on the Update Total button (see Fig 4).
3. The bottom component contains the score cutoff and the match button
 - a. Score Cutoff: The score cutoff value determines what match results are returned. Match results which have a score greater than or equal to the score cutoff will be returned. **Note :** the score cutoff value should not be higher than the highest possible score.
 - b. Select Objects to Match: Once the match criterion has been set the User can start the match process by pressing this button. When the button is pressed a window displaying all objects under the source class will be displayed.

Source Class : Sutures B Target Class : Sutures A

Sutures B:Sutures A:Default Add Remove **1**

Current Match Criterion: Sutures B:Sutures A:Default

Highest Possible Score: 22.00

Source Relationship	Target Relationship	Matching Function	Weight	Update Total
DF-USER PACKAGE INFO	AMDF-USER PACKAGI	Subset	x 1.0	2
RE NEEDLE POINT STYLE	ARMED SUTURE NEED	Equals	x 1.0	
SUTURE NEEDLE STYLE	ARMED SUTURE NEED	Equals	x 1.0	
COLOR	COLOR	Equals	x 1.0	
DIAMETER	DIAMETER	Compare Measures/5	x 1.0	
Description String	null	Equals	x 0.0	
END TYPE	END TYPE	Equals	x 1.0	
EYE STYLE	EYE STYLE	Equals	x 1.0	
FIGURE NUMBER	FIGURE NUMBER	Equals	x 1.0	
IGNORE	null	Equals	x 0.0	
ITEM NAME	ITEM NAME	Equals	x 1.0	
LENGTH	LENGTH	Compare Measures/5	x 1.0	
MANUFACTURER	MANUFACTURER	Equals	x 1.0	
MATERIAL AND LOCATION	MATERIAL AND LOCA	Equals	x 1.0	
LE DESIGN DESIGNATION	NEEDLE DESIGN DESI	Equals	x 1.0	
LE NOMINAL DIAMETER	NEEDLE NOMINAL DIA	Equals	x 1.0	

Score Cutoff : 4.0 **3**

Select Objects To Match

Fig 4

Selecting objects to match—

The object chooser window displays all the objects under the source class. The name and native id of these objects are displayed. The User can choose any number of objects to compare or can select all the objects are under the class. To select multiple objects use the ctrl and shift keys to select contiguous and noncontiguous objects. To match only the selected objects click on the Match Selected Objects button or to match all objects click on the Match All Objects button.

Select Objects : Demand Sutures:Commercial Sutures:Default

Edit

Object Name	Object Native Id
NSNs_for_SUTURES_(2_INCs)	6515000017682
NSNs_for_SUTURES_(2_INCs)	6515000448799
NSNs_for_SUTURES_(2_INCs)	6515000547444
NSNs_for_SUTURES_(2_INCs)	6515000547446
NSNs_for_SUTURES_(2_INCs)	6515000547451
NSNs_for_SUTURES_(2_INCs)	6515000547452
NSNs_for_SUTURES_(2_INCs)	6515000606504
NSNs_for_SUTURES_(2_INCs)	6515000678241
NSNs_for_SUTURES_(2_INCs)	6515000678242
NSNs_for_SUTURES_(2_INCs)	6515000678243
NSNs_for_SUTURES_(2_INCs)	6515000678244
NSNs_for_SUTURES_(2_INCs)	6515000741016
NSNs_for_SUTURES_(2_INCs)	6515000760337
NSNs_for_SUTURES_(2_INCs)	6515001017610
NSNs_for_SUTURES_(2_INCs)	6515001138337
NSNs_for_SUTURES_(2_INCs)	6515001138338
NSNs_for_SUTURES_(2_INCs)	6515001138339
NSNs_for_SUTURES_(2_INCs)	6515001138343
NSNs_for_SUTURES_(2_INCs)	6515001169103
NSNs_for_SUTURES_(2_INCs)	6515001194624
NSNs_for_SUTURES_(2_INCs)	6515001223866
NSNs_for_SUTURES_(2_INCs)	6515001395911
NSNs_for_SUTURES_(2_INCs)	6515001395916
NSNs_for_SUTURES_(2_INCs)	6515001395922

Match All Objects Match Selected Objects

Fig 5

Match Results –

The match results windows shows all the matches above the cutoff. Four different columns are displayed in this window:

- Native Id of the source object.
- The score of the best match.
- The number of target objects that matched.
- The number of target objects that attained the best score.

To save the results to a bar delimited flat file click on the Save to File button located at the bottom of the match results window. Matcher will prompt you specify the location where the results are to be saved. If the User chooses an existing file the he/she will be prompted before Matcher overwrites the contents of the file. To save the match results to an MS Access database table click on the Save to Db button located at the bottom of the window. Matcher will

prompt the User to specify the location of the Access Database and the name of the database table where the results are to be saved. If the table exists and its structure is compatible with that needed to save the results it will be appended, otherwise the user will be prompted to choose another table. If the table does not exist it will be created.

The User can also choose to view in detail what target attributes matched and see in graphical form the reasoning behind the score for a particular source object. To bring up the detail view, right click on the source object of interest and choose the View All Matching Target Objects option.

Match Results Sutures B:Sutures A:Default			
Edit			
Source Native Id	Best Score	Number of Results	Results with Best Score
1588H	6.0	66	2
1629H	6.0	55	2
1667G	6.0	54	2
1665G	6.0	59	1
1665H	6.0	56	1
1666H	6.0	49	1
1666G	6.0	49	1
1615G	6.0	45	1
1662G	6.0	41	1
1611G	6.0	32	1
1663H	5.0	48	9
1663G	5.0	48	9
1661G	5.0	39	3
1638H	5.0	27	2
1638G	5.0	27	2
1636G	5.0	22	2
1654G	5.0	28	1
1637G	5.0	27	1
1644G	5.0	20	1
1643G	5.0	20	1
1627G	5.0	19	1

Save To File

Save To Db

Fig 6

Detail Results window—

Like the right panel in the main window the detail results window is also composed of the three distinct components.

1. The top part of the window is used to display information about the source object. The name of the attributes, their values and the weights associated with each are displayed.

The highest possible score that can be achieved taking into account the weights is shown in the last line; in this case it is equal to 9.0.

2. The main part of the window displays the target objects that matched the source object, the total score of the match along with the values of attributes associated with the target objects. A color coding scheme is used to distinguish between values that were compared and matched, were compared and didn't match, and those that were not compared.
 - In this particular example the color green is associated with values that were compared and matched. In the example the first target object has the same length as the source object, 18.0 inches. The second value in this cell [1.0000] is the score associated with this match. This is equal to the value returned by the matching function (matching functions always return a value between -1.0 and 1.0) multiplied by the weight entered for the source relationship.
 - The color red is associated with values that were compared but did not match. Again looking at the first row the source and target object values for the "Size Designator" attribute don't match.
 - If the target object has a populated value for an attribute but the source object does not, no comparison occurs, e.g. "Needle Design Designation" attribute in the first row. The cell for this attribute is colored gray and the value of the target attribute is displayed with no score. If the reverse happens and the source object has a value and the target object does not as is the case for "Material and Location" attribute, the corresponding cell is left empty and colored gray.
 - It is often the case that for an attribute a target object may have multiple values. When this occurs a second row for the object is inserted into the table and the whole row is colored white. The second row in figure 7 is an example of this. One of these values is matched to by the matcher and the appropriate coloring is used. In this case the second value for the "Needle Type Designator" attribute is compared and a score of [-1.0000] is assigned.
3. The colors used for these different situations can be changed at any time by using the drop down boxes in section 3 of the window. They can also be changed using the Set Colors menu item located in the Matcher menu in the main window.

Matcher v0.99alpha - C:\wsb\sys\XSB\CVS\apps\weave\oms_matcher\matcher_gui\suture_oms

File Windows Help Matcher

← Detailed Results for 1665G

Source Class : Batch-ESURO_HARVEST
Source Object : 1665G

1

ARMED SUTURE NEEDLE POINT STYLE : REVERSE CUTTING EDGE : 1.0
ARMED SUTURE NEEDLE STYLE : 3/8 CIRCLE : 1.0
LENGTH : 18.0 INCHES NOMINAL : 1.0
STRAND FIBER ARRANGEMENT : MONOFILAMENT : 1.0
COLOR : BLACK : 1.0
SIZE DESIGNATOR : 6-0 : 1.0
MATERIAL AND LOCATION : NYLON : 1.0
ITEM NAME : RE, NONABSORBABLE, SURGICAL : 1.0
NEEDLE TYPE DESIGNATOR : PB-3 : 1.0

Weights Total : Highest possible score : 9.0

Score	Target Object	COLOR	ITEM NAME	LENGTH	MATERIAL AN	NEEDLE DESIGN	NEEDLE TYP	SIZE DESIGN
1.0	851501055022					PLASTIC SURGERY	P-3	
1.0	851501055022					CUTICULAR		
1.0	851501045443					SUTUPAK		
1.0	851501045443							
1.0	851501040081					PLASTIC SURGERY		
1.0	851501040081							
1.0	851501030200							
1.0	851500982715							
1.0	851500987598							
1.0	851500944987					PLASTIC SURGERY		
1.0	851500944987							
1.0	851500917583							
1.0	851500917583							
1.0	851500805147							
1.0	851500805147							
1.0	851500823784							

2

Match : No Comparison : No Match :
green yellow red

3

Fig 7

Adding a new class to the OMS –

The generic matcher provides some rudimentary OMS editing functions. One of these is the ability to add a new class to the OMS. To add a class, select the node, under which you want the new class to appear, right click and choose the "Modify OMS/Add a new Class" option from the pop up menu. Generic Matcher will prompt the User to enter the name, native id and source of the new class. The User has the option to make the new class a parameterized class. This is done by checking the box next to the "Parameterized Class" label and entering the arity of the class below it. If the new class is a parameterized class the use will be prompted to choose from the existing concepts in the OMS the arguments of the class.

If the class was added successfully it will appear under the parent node when you click ok.

Edit

Class Name :

Native ID :

Source : oms_matcher

Parameterized Class : ☐

Arity :

OK Cancel

Fig 8

Adding a new relationship –

Along with the ability to add a new class to the OMS, the Matcher provides the ability to add relationships to the class. To start this process select the class you want to modify, right click on the node and select the “Modify OMS/Add a new Relationship” option. The User will be prompted to the name of the new relationship. The User must also specify the type of the relationship, i.e. what type of values will this relationship have e.g. string, number, measure etc. To verify whether the new relationship was added properly you can always view the relationships attached to a class by right clicking on the node and selecting the View Relationship option.

Edit

Relationship Name :

Relationship Type : String ▼

OK Cancel

Fig 9

Importing objects into the OMS –

The Generic Matcher provides the ability to import objects from either a delimited file or MS Access table. To start the process right click on the node under which you want the objects inserted. Select the Import Objects from File/Db option; Matcher will prompt you to select the batch file or Access database file. Navigate through the directory structure and click on the “Import” button to load the file into the Matcher.

To load files from a Access select the database file (*.mdb), Matcher will prompt the User to enter the name of the database table from which to import the objects. Otherwise the User will be prompted to select a column delimiter for the batch text file to be loaded into the Matcher. The User will have the option of choosing from pipe, comma, colon, and tab as possible file delimiters (see Figure 10). Once the appropriate delimiter has been selected, the User should press the Ok button to prompt the Matcher to load the batch file.

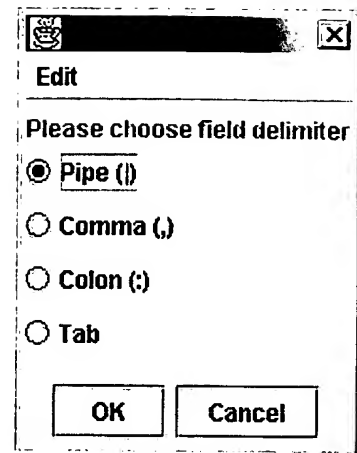


Fig 10

An editor will now be displayed, allowing the User to select which columns of the batch file or fields from the database table they want imported. Under the First Line/Title heading, the User will see a list of all of the names or titles of the columns in the text file (It is assumed that first row of the file contains column names separated by a pre-selected file delimiter). The User will now need to select appropriate designations for each of these columns from the drop down list found under the Relationships heading. The Relationship designations for each column are essentially a set of instructions on how the Matcher should handle the information contained within the column. To select a Relationship designation for an attribute, the User must triple click on the drop down box in the Relationships column and select one of the options displayed.

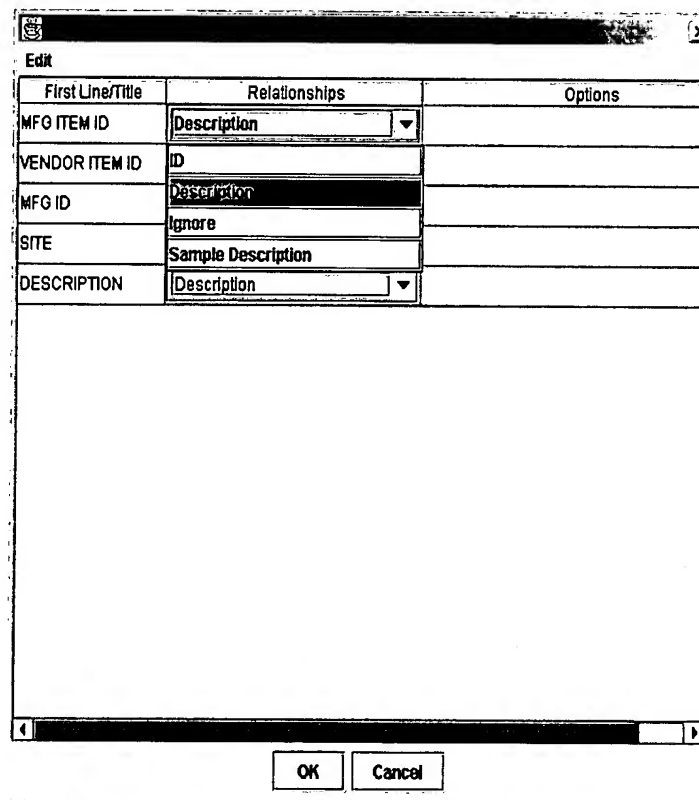


Fig 11

Editing User preferences –

Matcher provides a central location where preferences can be managed. To edit preferences select the Edit Preferences menu item under the Matcher menu. A dialog box will appear listing the various options that can be set. Once you have set all the options simply close the dialog box. All the User specified preferences are saved in the prefs file located in the application directory; it is recommended that the User not edit this file.

- **OMS Load Dir:** This is the directory to which Matcher opens the file dialog when the User uses the Load OMS or Merge OMS options.
- **OMS Startup Dir:** The User can specify for an OMS to be loaded by default each time the matcher starts up.
- **Previous Match Results:** Whenever a match is executed in the generic matcher information regarding scores is added to the OMS as an attribute of the source object. If you wish not to save this information choose this option. It is important to note that this option causes adverse effects if any result windows are open when saving occurs.
- **Scoring Information:** By default when matcher saves match results the individual scores assigned to object attributes are not saved. If the user chooses this option the scoring information will be saved along with the attribute values.
- **Maximize @Startup:** Option to maximize the window at startup.
- **Hide System Nodes:** Option to hide class nodes in the source and target trees for concepts that have a system source, e.g. OMS, TMS, ODE, ODC etc. .

Another selection available under the “Matcher” menu is the option to “Write Results directly to file.” When this option is selected the results window will not appear when a match is completed instead the user will be asked whether he/she wants to save the results to a file or a database.

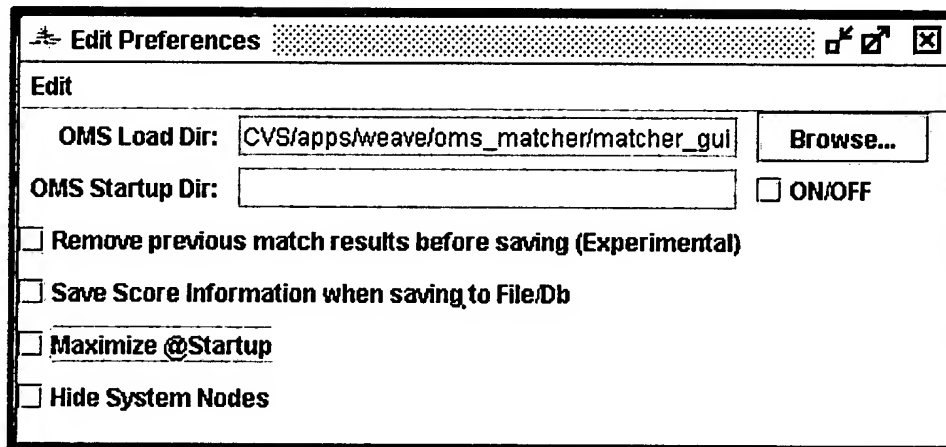


Fig 12

Help Browser—

Generic matcher provides built in help features including the help browser. The help browser allows the user to view application documentation and view answers to frequently asked

questions. To invoke the help browser simply click on the Help Contents menu item under the Help menu. The help browser is very similar to an internet browser and provides quick answers to questions.

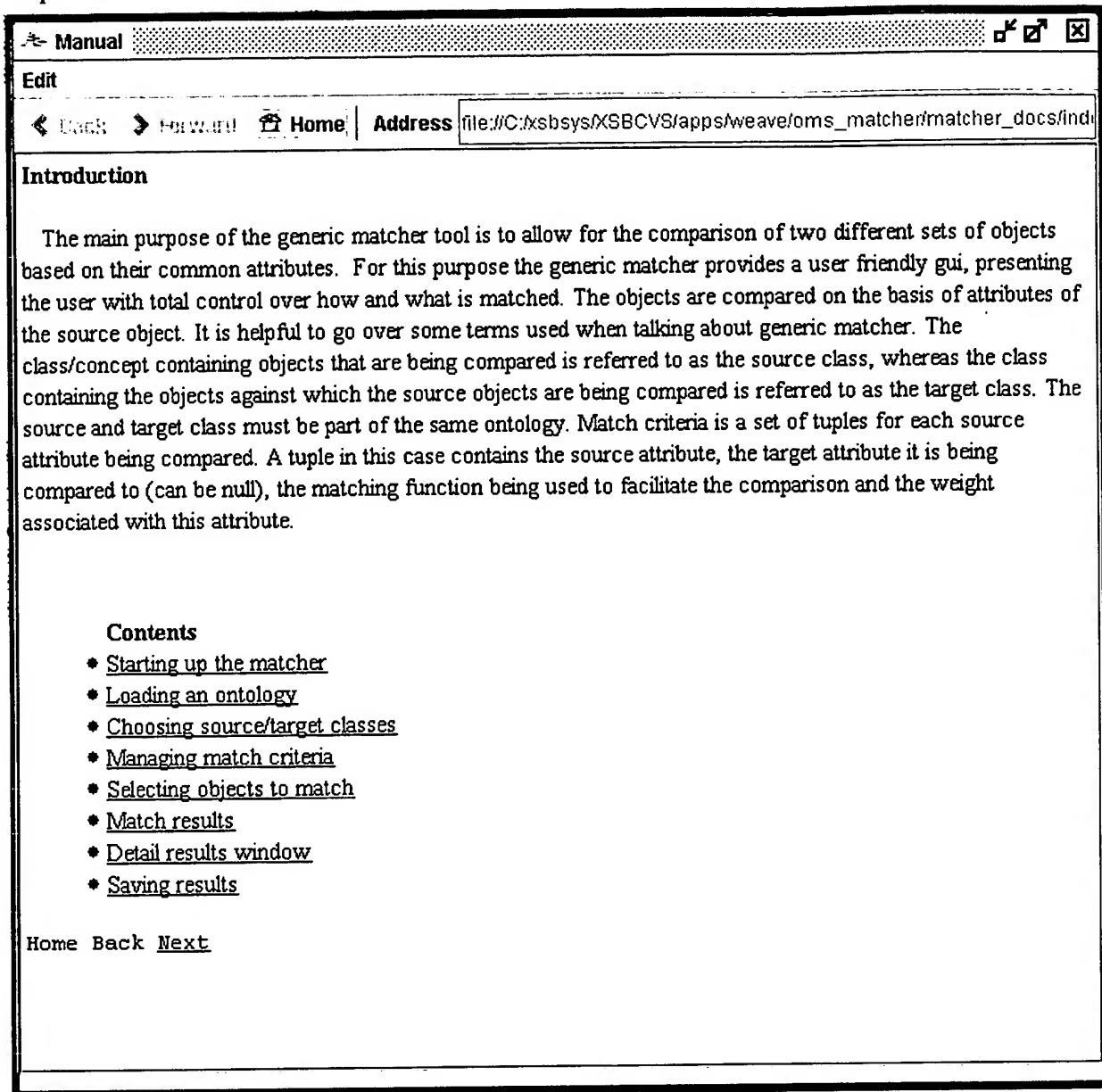


Fig 13

Matching function descriptions

To view a description about the available matching functions, along with how they handle scoring click on the Function Descriptions menu item under the Help menu. This feature provides information about every matching function that is currently bundled with the Matcher and have been loaded.

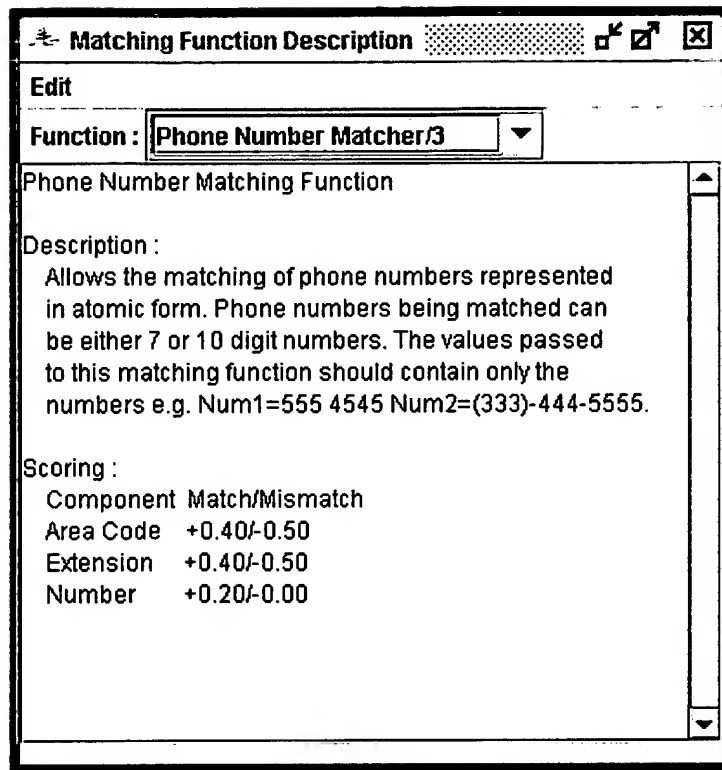


Fig 14

5.2 Related Processing

When the User selects a pair of source and target classes in a session, the Matcher will run background processing in order to generate or load default match criteria; this may cause a delay for the User as they will have to wait several seconds for the background processing to be completed.

5.3 Data Backup

Normal database management backup procedures should be used in conjunction with the Generic Matcher software; users should be careful to back up the OMS directory used for saving the intermediate state of the Generic Matcher as well as input and output data as part of their routine backup procedure.

5.4 Recovery from Errors, Malfunctions and Emergencies

Should your software malfunction or should you encounter an error that prevents you from continuing to use the software as prescribed in this manual, contact technical support immediately at 631-444-6800 or via email at support@xsb.com.

A - Glossary:

Class - (sometimes referred to as a node or a concept) a set containing members regarded as having certain relationships in common, a kind or category.

Match Criterion – the source and target class, the set of attributes being compared, the weights and matching function associated with each attribute and the score cutoff all together form the match criterion.

Matching Function – specialized prolog predicate used by the matcher to compare two values of a particular data type. Matching functions always return a value between [-1.0,+1.0].

OMS - ontology management system to manage and store ontology-based knowledge.

Parameterized Class – represents an infinite set of Values such as integers, measures and so on. For example, number of Stents in a package may be any integer – we can not name all of the possible Values.

Source Class – the class in the ontology containing the set of objects that are currently being compared.

Target Class – the class in the ontology containing the set of objects that the source objects are being compared against.

Source Object – a member of the source class.

Target Object – a member of the target class.

B - Third-party Software Credits

The Generic Matcher makes use of several third-party software packages. Some of these are recognized below.

- This product includes code licensed JRE v 1.4 by SUN Microsystems
- This product makes use of the open source XSB code
- This product makes use of the Java Look and Feel Repository

The developers of these third-party software programs do not warrant their software in any way. See the dist and lib directories for more information about these software programs and their licenses.